

SEQUENCE LISTING

<110> Ottawa Health Research Institute

<120> Diabetogenic Epitopes

<130> 08899427WO

<140> Unknown

<141> Unknown

<150> US 60/535,278

<151> 2004-01-09

<160> 8

<210> 1

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> epitope

<400> 1

Glu Glu Gln Leu Arg Glu Leu Arg Arg Gln
1 5 10

<210> 2

<211> 2018

<212> DNA

<213> unknown

<220>

<223> wheat gene

<400> 2

atggcgacca	gaggcagagc	aaccatccct	cttcattttcc	tcttgggcac	aaggcttttc	60
ttccgcgcgg	ctgtttccgc	ctcccatgac	gaggaggagg	acaggcgcgg	tgggcgtctcg	120
cttcagcgggt	gcgtgcagcg	gtgccagcag	gacggccgcgc	ggtactctca	tgcggcgtgc	180
gtgcaggagt	gcggggacga	ccagcagcag	cacgaaaggc	acgaggcagg	ggagcaggcgc	240
cgcgccatg	gcgggcacgc	cgagggggag	cgtgaggagg	agcaggccgc	tggccgtggg	300
cgggcgcc	agggagagcg	tgaggaggag	cagggccgtg	gacgtgggcg	gcgcggcgcag	360
ggagagcgtg	atgaggagca	cggggatggc	cggcgccgt	acgtgtttag	cccgccgcgc	420

ttccgcggca tcatccggag cgaccacggg ttctgtcaagg cccttcggcc gttcgacgaa	480
gtgtccaggc tcctccgggg catcaggaac tacccgtgtcg ccatcatgga ggtgaaccgg	540
cgcgcgttcc tgggtccgggg actcacggac gcagacggcg tgggtctaact cgctcaaggc	600
gagggggtgc tgacgggtat cgagaacggc gagaaggcggt cctacacccgt caggcaaggc	660
gatgtgtatcg tggggccggc ggggtccatc atgcacccgtt ccaacacccga cggccggagg	720
aagctggta tcgccaagat tctccacacc atctccgtcc cccggcaagtt ccagtatttc	780
tcggccaaagg ctctccctgc tagtttgagc aaacgggtgc tcacagggc gttaaagacc	840
tcggatggcggc ggctgggttag tctcttgggc agcogccaa gcaaggaggaa ggaggaggaaag	900
tccatctcca tctgtccgcgc gtcagaggagc cagtcggcg agctgogtgc ccaggcggtcc	960
gagggtgtacc agggccacca ctggcccttc ccccocttcc gccggcgactc gcccggacacc	1020
ttcaacctcc tggagcagcg ccccaagatc gccaacccgc atggccggct ctacgaggcc	1080
gacgccccgtt gcttccacgc cctcgcccaa cacgacgtcc gctgtccgggtt ggccaaacatc	1140
acgcgggggtt ctatgaccgcg gcccatacttcc aacaccaggat cgttcaagttt cggccgttgt	1200
cttggaaaggcg agggcgagggtt ggagatgttc tgcccgccacc tggcgcggcga cagcggcgcc	1260
cgcgcggcaag .agcacggcaaa gggcagggtgg aggagcgagg aagaggaggaa cgaccggcg	1320
cagcaacggcc gacgccccgtt cggctccaggat tggaggaggaa agcaggacca gcaagggttt	1380
cagacgggtcc ggcggccgggtt gtagccggccg tgggggttcc tgggtccccc cggccaccccg	1440
gtgggtggaga tggctctgttcc cccggccggc acgcaacctcc aggtgggtgtt ctccggatcc	1500
aacgcggaga ggaacggcg ggtgtggctt ccggggaggaa acaacgttat cggccaggctt	1560
gacgaccccgccc cccaggaggat ccccttccggcc accggccggcga gggagggttcc ggagggttcc	1620
cgcgcggcaagg atcagcaggatcc cgggggttcc tggccggaccc cccggccggc gcaaggaggat	1680
gagcgccgggg accggccggcc tgggtggccgc gggccggccgc acggaaaggccgtt ggagggttcc	1740
ctggaggatgg caacggccgcg cttctggatcc ggcggccggcgttgggtttaa gtgtatgtgtt	1800
gagctggaggcc cccggccggcatt tggaggatgttcc atttggatgtt gtgtgtttaaatgttcc	1860
gcggggaggatcc cataaataaag tgggtggccgc ggcggccggcgttgggtttaa gtgtatgtgtt	1920
taccccttccatcc caaggccatgc atggccaaaca taaaataaaca caagggggttcc ggcgttcc	1980
ttcagtaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa	2018

<210> 3
<211> 588
<212> PRT
<213> unknown

<220>
<223> WP5212 sequence

<400> 3

Met Ala Thr Arg Gly Arg Ala Thr Ile Pro Leu Leu Phe Leu Leu Gly
1 5 10 15

Thr Ser Leu Leu Phe Ala Ala Ala Val Ser Ala Ser His Asp Glu Glu
20 25 30

Glu Asp Arg Arg Gly Gly Arg Ser Leu Gln Arg Cys Val Gln Arg Cys
35 40 45

Gln Gln Asp Arg Pro Arg Tyr Ser His Ala Arg Cys Val Gln Glu Cys
50 55 60

Arg Asp Asp Gln Gln His Gly Arg His Glu Gln Glu Glu Gln Gly
65 70 75 80

Arg Gly His Gly Arg His Gly Glu Gly Glu Arg Glu Glu Glu Gln Gly
85 90 95

Arg Gly Arg Gly Arg Arg Gly Gln Gly Glu Arg Glu Glu Glu Gln Gly
100 105 110

Arg Gly Arg Gly Arg Arg Gly Glu Gly Glu Arg Asp Glu Glu His Gly
115 120 125

Asp Gly Arg Arg Pro Tyr Val Phe Gly Pro Arg Ser Phe Arg Arg Ile
130 135 140

Ile Arg Ser Asp His Gly Phe Val Lys Ala Leu Arg Pro Phe Asp Glu
145 150 155 160

Val Ser Arg Leu Arg Gly Ile Arg Asn Tyr Arg Val Ala Ile Met
165 170 175

Glu Val Asn Pro Arg Ala Phe Val Val Pro Gly Leu Thr Asp Ala Asp
180 185 190

Gly Val Gly Tyr Val Ala Gln Gly Glu Gly Val Leu Thr Val Ile Glu
195 200 205

Asn Gly Glu Lys Arg Ser Tyr Thr Val Arg Gln Gly Asp Val Ile Val
210 215 220

Ala Pro Ala Gly Ser Ile Met His Leu Ala Asn Thr Asp Gly Arg Arg
225 230 235 240

Lys Leu Val Ile Ala Lys Ile Leu His Thr Ile Ser Val Pro Gly Lys
 245 250 255

Phe Gln Tyr Phe Ser Ala Lys Pro Leu Leu Ala Ser Leu Ser Lys Arg
 260 265 270

Val Leu Thr Ala Ala Leu Lys Thr Ser Asp Glu Arg Leu Gly Ser Leu
 275 280 285

Leu Gly Ser Arg Gln Gly Lys Glu Glu Glu Glu Lys Ser Ile Ser Ile
 290 295 300

Val Arg Ala Ser Glu Glu Gln Leu Arg Glu Leu Arg Arg Gln Ala Ser
 305 310 315 320

Glu Gly Asp Gln Gly His His Trp Pro Leu Pro Pro Phe Arg Gly Asp
 325 330 335

Ser Arg Asp Thr Phe Asn Leu Leu Glu Gln Arg Pro Lys Ile Ala Asn
 340 345 350

Arg His Gly Arg Leu Tyr Glu Ala Asp Ala Arg Ser Phe His Ala Leu
 355 360 365

Ala Gln His Asp Val Arg Val Ala Val Ala Asn Ile Thr Pro Gly Ser
 370 375 380

Met Thr Ala Pro Tyr Leu Asn Thr Gln Ser Phe Lys Leu Ala Val Val
 385 390 395 400

Leu Glu Gly Glu Gly Glu Val Glu Ile Val Cys Pro His Leu Gly Arg
 405 410 415

Asp Ser Glu Arg Arg Glu Gln Glu His Gly Lys Gly Arg Trp Arg Ser
 420 425 430

Glu Glu Glu Glu Asp Asp Arg Arg Gln Gln Arg Arg Arg Gly Ser Gly
 435 440 445

Ser Glu Ser Glu Glu Glu Gln Asp Gln Gln Arg Tyr Glu Thr Val Arg
 450 455 460

Ala Arg Val Ser Arg Gly Ser Ala Phe Val Val Pro Pro Gly His Pro
 465 470 475 480

Val Val Glu Ile Ala Ser Ser Arg Gly Ser Ser Asn Leu Gln Val Val
 485 490 495

Cys Phe Glu Ile Asn Ala Glu Arg Asn Glu Arg Val Trp Leu Ala Gly
 500 505 510

Arg Asn Asn Val Ile Ala Lys Leu Asp Asp Pro Ala Gln Glu Leu Ala
 515 520 525

Phe Gly Arg Pro Ala Arg Glu Val Gln Glu Val Phe Arg Ala Lys Asp

530

535

540

Gln Gln Asp Glu Gly Phe Val Ala Gly Pro Glu Gln Gln Gln Glu His
 545 550 555 560

Glu Arg Gly Asp Arg Arg Arg Gly Asp Arg Gly Arg Gly Asp Glu Ala
 565 570 575

Val Glu Ala Phe Leu Arg Met Ala Thr Ala Ala Leu
 580 585

<210> 4

<211> 290

<212> PRT

<213> unknown

<220>

<223> alpha/beta gliadin A-II precursor

<400> 4

Met Lys Thr Phe Pro Ile Leu Ala Leu Leu Ala Ile Val Ala Thr Thr
 1 5 10 15

Ala Thr Thr Ala Val Arg Val Pro Val Pro Gln Leu Gln Leu Gln Asn
 20 25 30

Pro Ser Gln Gln Gln Pro Gln Glu Gln Val Pro Leu Val Gln Glu Gln
 35 40 45

Gln Phe Gln Gly Gln Gln Gln Pro Phe Pro Pro Gln Gln Pro Tyr Pro
 50 55 60

Gln Pro Gln Pro Phe Pro Ser Gln Gln Pro Tyr Leu Gln Leu Gln Pro
 65 70 75 80

Phe Pro Gln Pro Gln Leu Pro Tyr Pro Gln Pro Gln Pro Phe Arg Pro
 85 90 95

Gln Gln Pro Tyr Pro Gln Pro Gln Pro Gln Tyr Ser Gln Pro Gln Gln
 100 105 110

Pro Ile Ser Gln
 115 120 125

Gln Gln Ile Leu Gln Gln Ile Leu Gln Gln Gln Ile Pro Cys Arg
 130 135 140

Asp Val Val Leu Gln Gln His Asn Ile Ala His Gly Ser Ser Gln Val
 145 150 155 160

Leu Gln Glu Ser Thr Tyr Gln Leu Val Gln Gln Leu Cys Cys Gln Gln
 165 170 175

Leu Trp Gln Ile Pro Glu Gln Ser Arg Cys Gln Ala Ile His Asn Val
 180 185 190

Val His Ala Ile Ile Leu His Gln Gln His His His His Gln Gln Gln
 195 200 205

Gln Gln Gln Gln Gln Gln Pro Leu Ser Gln Val Ser Phe Gln Gln
 210 215 220

Pro Gln Gln Gln Tyr Pro Ser Gly Gln Gly Phe Phe Gln Pro Ser Gln
 225 230 235 240

Gln Asn Pro Gln Ala Gln Gly Ser Phe Gln Pro Gln Gln Leu Pro Gln
 245 250 255

Phe Glu Glu Ile Arg Asn Leu Ala Leu Gln Thr Leu Pro Ala Met Cys
 260 265 270

Asn Val Tyr Ile Pro Pro Tyr Cys Thr Ile Ala Pro Phe Gly Ile Phe
 275 280 285

Gly Thr
 290

<210> 5

<211> 307

<212> PRT

<213> unknown

<220>

<223> alpha/beta gliadin MM1 precursor

<400> 5

Met Lys Thr Phe Leu Ile Leu Ala Leu Leu Ala Ile Val Ala Thr Thr
 1 5 10 15

Ala Arg Ile Ala Val Arg Val Pro Val Pro Gln Leu Gln Pro Gln Asn
 20 25 30

Pro Ser Gln Gln Gln Pro Gln Glu Gln Val Pro Leu Val Gln Gln Gln
 35 40 45

Gln Phe Pro Gly Gln Gln Gln Pro Phe Pro Pro Gln Gln Pro Tyr Pro
 50 55 60

Gln Pro Gln Pro Phe Pro Ser Gln Gln Pro Tyr Leu Gln Leu Gln Pro
 65 70 75 80

Phe Pro Gln Pro Gln Leu Pro Tyr Pro Gln Pro Gln Leu Pro Tyr Pro
 85 90 95

Gln Pro Gln Leu Pro Tyr Pro Gln Pro Gln Pro Phe Arg Pro Gln Gln
 100 105 110

Pro Tyr Pro Gln Ser Gln Pro Gln Tyr Ser Gln Pro Gln Gln Pro Ile
 115 120 125
 Ser Gln Gln Gln Gln Gln Gln Gln Gln Gln Lys Gln Gln
 130 135 140
 Gln Gln Gln Gln Gln Ile Leu Gln Gln Ile Leu Gln Gln Leu
 145 150 155 160
 Ile Pro Cys Arg Asp Val Val Leu Gln Gln His Ser Ile Ala Tyr Gly
 165 170 175
 Ser Ser Gln Val Leu Gln Gln Ser Thr Tyr Gln Leu Val Gln Gln Leu
 180 185 190
 Cys Cys Gln Gln Leu Trp Gln Ile Pro Glu Gln Ser Arg Cys Gln Ala
 195 200 205
 Ile His Asn Val Val His Ala Ile Ile Leu His Gln Gln Gln Gln
 210 215 220
 Gln Gln Gln Gln Gln Gln Pro Leu Ser Gln Val Ser Phe Gln Gln
 225 230 235 240
 Pro Gln Gln Gln Tyr Pro Ser Gly Gln Gly Ser Phe Gln Pro Ser Gln
 245 250 255
 Gln Asn Pro Gln Ala Gln Gly Ser Val Gln Pro Gln Gln Leu Pro Gln
 260 265 270
 Phe Glu Glu Ile Arg Asn Leu Ala Leu Glu Thr Leu Pro Ala Met Cys
 275 280 285
 Asn Val Tyr Ile Pro Pro Tyr Cys Thr Ile Ala Pro Val Gly Ile Phe
 290 295 300
 Gly Thr Asn
 305

<210> 6
 <211> 20
 <212> PRT
 <213> unknown

<220>
 <223> diabetogenic epitope homopolymer

<400> 6

Glu Glu Gln Leu Arg Glu Leu Arg Arg Gln Glu Glu Gln Leu Arg Glu
 1 5 10 15

Leu Arg Arg Gln

20

<210> 7

<211> 18

<212> DNA

<213> artificial

<220>

<223> primer

<400> 7

accacgggtt cgtcaagg

18

<210> 8

<211> 18

<212> DNA

<213> artificial

<220>

<223> primer

<400> 8

aacacctcct gcacctcc

18